

200

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 MRGYYCFPRFLVSVLFLHVHGCRSQTCDPTDIAALAAASDGLDTKAAGMVG-WGPGDAACCSMTQVSC-DLG-RVVALDLSNRSSLSRNLRGGAEVARAGRPLSHRRRLDSANCAGAACPAAGG-FPAIEVVNVSNQFTCPRAF-PGA
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 MRELEMSCHVVSG-VLVFLVLAATICCCACACVEVPRKALLTADAAACRADCYIWEWQSPDCCWMDVCGG-GDGEVIRLHPPRGLOGGTXSPSIGNLTGLTHLNLSNQELAG-QPPEVLFSLPNVTVDVSYNLSGELSVATGAAA-RGGLSLEVLDWSNLLAQCFSAIWEIT
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 AK068495.q MQLNPNCSSSSSTTTTTKLSVAFFRLLVILLSFASPTSSCTEQEPSSIGLECLGPPGHNGSSTSWSVKIDCCRKEINGSDGTVDVTDVSLASQGLOGRISPGLNLTGLLHNLSNLLNG-YPMLPILFSRHTIVDVSFNNLIDGSLPE-LESPSG-GSELOVNLNISNLFQGIFESKQWEVM
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 2phk_Phk
 lias_TGFBR

400

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 AK109928.p -MNGSSCDGPVFCGCKLJNDFLDGNGLTCGKPLDLYMPARLKSLQBNKSGC-SLDDDDGNTETCCHDLSYMFNINIDPVEVKRSLESINASLNSQNLGPLSLLSCPCMRLVVSURNNNSLGEITIDCRLLTFLNNRDFGATNKLRCADPRAASCER
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 AK13166.q -ANANYYLIG-AAVPRANPFHNGIDPFTSFCVNLIEHICLGMALTNQEDPLFHILKRNLLCQIQBRSUO-SLSRERPRNNSVSLVDRDVWFLFSEBDPDPVDELIQKFLGQNGFICGIPKSLANSNSLNENLNRRNNSLSCRUM-NCNTMAIASLDDGNTENRGRFENPDKRUK
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 AK110293.q -MKLKEPLPLANNNTGKPLGALSNSWTSLSRIDEIDLRSNFVQDITVWDFSLANLTVEFDVASNFNGETGTPPSYTCOTDJK
 AK110462.q PRLVSLNSNSNSGKTHIPS-ICVSCPALAVLDSLNVNLSQCVISPLFCNCNSLRFVSAGRNNTLCEGLDGLDFVKAQOBHEPDLGECODLHD-ESENKATVNLIDVLLDQGKPLGKESLTSKMEKPLRBLANNNTGKPLGALSNSWTSLSRIDEIDLRSNFVQDITVWDFSLANLTVEFDVASNFNGETGTPPSYTCOTDJK
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 2phk_Phk
 lias_TGFBR

600

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 1ir3_IRK
 2phk_Phk
 lias_TGFBR

1210 1220 1230 1240 1250 1260 1270 1280 1290

AK068495.q|.....|.....|.....|.....|.....|.....|.....|.....|.....|...

83525390.q

AK109928.q

15227264.q

AK103166.q

51040021.q

AK110293.q

AK110462.q

51040019.q

25070011.q

25070012.q

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25070010.q

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